SPLICE FORM 1:

```
   1 CGTCCTTCCT GGTCCTGCGG GTCCAGGACT GTCCGCGGGG TTGAGGGAAG
  51 GGGCCGTGCC CGGTGCCAGC CCAGGTGCTC GCGGCCTGGC TCCATGGCCC
 101 TGGTCACAGT GAGCCGTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCGTG
 151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
 201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCCT GGGACTGCAG GATGGAGGGG
 251 ACAATGATGA TGCAGCAGAG GCCAGTTCTG AGCCAACAGA GAAGGCCCCG
 301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
 351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
 401 AGCTGCTGAG GCCGCAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
 451 CCCCGGCCTC CCCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
 501 AGAAGGTCTG AGCCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCCTG
 551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
 601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
 651 TGGGCAAAGC CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
 701 CACTCCAGGT ATTGCACCAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
 751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
 801 GAACTCCGAA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
 851 AGTCTCTGCG GCCTCCCAGC GCCGAGCCTG GCGGGTCCTC AGAACAGGAG
 901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
 951 TGACCTGGAG AGTGTCACTT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
1051 CTGCTGCTGG TGGCACAGCG GGACCGAGCC TCCCGCATCT TCCCCCACCT
1101 CTACCTGGGC TCAGAGTGGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
1151 ACAGGGTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
1251 CCAGCTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
1301 GAGCACAGGG CACCCACGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
1351 TCAGCGGCCA CAGTGCTGGC CTATGCCATG AAGCAGTACG AATGCAGCCT
1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCCATC GCCCGCCCCA
1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
1501 AGAACCTGAG GGTGGTGGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
1601 GGGGTCATGA GGTCCATCAG TCTTCTGGAG CCCTCCTTGG AGCTGGAGAG
1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTTCTCTTCC CACGAGTCTT
1701 CACATGAAGA GCCTCTGCAG CCCTTCCCAC AGCTTGCAAG GACCAAGGGA
1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
1901 TCCTCTACGC CCAGGTTCCG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
1951 CAGTGGAGAG GAGGGCGAGG CCTGAGCCCT CACACATGCC CACGCTCCCC
2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
2051 TGCCGCACAC ATTCCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
2101 ACCTCCACC CCTGTCACTA CGGCCTCACC TCCCACCCCT GTCACTACAG
2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
2251 GGGGCAACAG CACCCTAGTT TCATTCTCAA CTCTAGCCCT GCACACTCAC
2301 CTGTGGCACG GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTCACGCCT
2351 CCCACCCCCG CCCCCTCCCT GCACCTCCTG TCCTCTCCCA GTTCATTCCT
2401 GGAACCAGCC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
2451 TCAGGCCCCA GCCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCCAGA CCTCCTGTGA
2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTTGTC
2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTTCA TAGCCTTACA GTATCTGGCT
2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
2701 AAAA
```

FEATURES:
5' UTR: 1-93
Start: 94-1506
Stop: 1509
3' UTR: 1510-2704

FIGURE 1, page 1 of 5

SPLICE FORM 2:

```
   1  TGGTTGAGGG AAGGGGCCGT GCCCGGTGCC AGCCCAGGTG CTCGCGGCCT
  51  GGCTCCATGG CCCTGGTCAC AGTGAGCCGT TCGCCCCCGG GCAGCGGCGC
 101  CTCCACGCCC GTGGGGCCCT GGGACCAGGC GGTCCAGCGA AGGAGTCGAC
 151  TCCAGCGAAG GCAGAGCTTT GCGGTGCTCC GTGGGGCTGT CCTGGGACTG
 201  CAGGATGGAG GGGACAATGA TGATGCAGCA GAGGCCAGTT CTGAGCCAAC
 251  AGAGAAGGCC CCGAGTGAGG AGGAGCTCCA CGGGGACCAG ACAGACTTCG
 301  GGCAAGGATC CCAGAGTCCC CAGAAGCAGG AGGAGCAGAG GCAGCACCTG
 351  CACCTCATGG TACAGCTGCT GAGGCCGCAG GATGACATCC GCCTGGCAGC
 401  CCAGCTGGAG GCACCCCGGC CTCCCCGGCT CCGCTACCTG CTGGTAGTTT
 451  CTACACGAGA AGGAGAAGGT CTGAGCCAGG ATGAGACGGT CCTCCTGGGC
 501  GTGGATTTCC CTGACAGCAG CTCCCCCAGC TGCACCCTGG GCCTGGTCTT
 551  GCCCCTCTGG AGTGACACCC AGGTGTACTT AGATGGAGAC GGGGGCTTCA
 601  GCGTGACGTC TGGTGGGCAA AGCGGATCT TCAAGCCCAT CTCCATCCAG
 651  ACCATGTGGG CCACACTCCA GGTATTGCAC CAAGCATGTG AGGCAGCTCT
 701  AGGCAGCGGC CTTGTACCGG GTGGCAGTGC CCTCACCTGG GCCAGCCACT
 751  ACCAGGAGAG ACTGAACTCC GAACAGAGCT GCCTCAATGA GTGGACGGCT
 801  ATGGCCGACC TGGAGTCTCT GCGGCCTCCC AGCGCCGAGC CTGGCGGGTC
 851  CTCAGAACAG GAGCAGATGG AGCAGGCGAT CCGTGCTGAG CTGTGGAAAG
 901  TGTTGGATGT CAGTGACCTG GAGAGTGTCA CTTCCAAAGA GATCCGCCAG
 951  GCTCTGGAGC TGCGCCTGGG GCTCCCCCTC CAGCAGTACC GTGACTTCAT
1001  CGACAACCAG ATGCTGCTGC TGGTGGCACA GCGGGACCGA GCCTCCCGCA
1051  TCTTCCCCCA CCTCTACCTG GGCTCAGAGT GGAACGCAGC AAACCTGGAG
1101  GAGCTGCAGA GGAACAGGGT CACCCACATC TTGAACATGG CCCGGGAGAT
1151  TGACAACTTC TACCCTGAGC GCTTCACCTA CCACAATGTG CGCCTCTGGG
1201  ATGAGGAGTC GGCCCAGCTG CTGCCGCACT GGAAGGAGAC GCACCGCTTC
1251  ATTGAGGCTG CAAGAGCACA GGGCACCCAC GTGCTGGTCC ACTGCAAGAT
1301  GGGCGTCAGC CGCTCAGCGG CCACAGTGCT GGCCTATGCC ATGAAGCAGT
1351  ACGAATGCAG CCTGGAGCAG GCCCTGCGCC ACGTGCAGGA GCTCCGGCCC
1401  ATCGCCCGCC CCAACCCTGG CTTCCTGCGC CAGCTGCAGA TCTACCAGGG
1451  CATCCTGACG GCCAGCCGCC AGAGCCATGT CTGGGAGCAG AAAGTGGGTG
1501  GGGTCTCCCC AGAGGAGCAC CCAGCCCCTG AAGTCTCTAC ACCATTCCCA
1551  CTTCTTCCGC CAGAACCTGA GGGTGGTGGG GAGGAGAAGG TTGTAGGCAT
1601  GGAAGAGAGC CAGGCAGCCC CGAAAGAAGA GCCTGGGCCA CGGCCACGTA
1651  TAAACCTCCG AGGGGTCATG AGGTCCATCA GTCTTCTGGA GCCCTCCTTG
1701  GAGCTGGAGA GCACCTCAGA GACCAGTGAC ATGCCAGAGG TCTTCTCTTC
1751  CCACGAGTCT TCACATGAAG AGCCTCTGCA GCCCTTCCCA CAGCTTGCAA
1801  GGACCAAGGG AGGCCAGCAG GTGGACAGGG GGCCTCAGCC TGCCCTGAAG
1851  TCCCGCCAGT CAGTGGTTAC CCTCCAGGGC AGTGCCGTGG TGGCCAACCG
1901  GACCCAGGCC TTCCAGGAGC AGGAGCAGGG GCAGGGGCAG GGGCAGGGAG
1951  AGCCCTGCAT TTCCTCTACG CCCAGGTTCC GGAAGGTGGT GAGACAGGCC
2001  AGCGTGCATG ACAGTGGAGA GGAGGGCGAG GCCTGAGCCC TCACACATGC
2051  CCACGCTCCC CTGACACTGA AGAGGATCCA CAACTCCTTG GAGAAACACC
2101  CTCACGTCTG TTGCCGCACA CATTCCTCTC AGCTCCGCCC CATACCCGTC
2151  ACTACAGCCT CACCTCCCAC CCCTGTCACT ACGGCCTCAC CTCCCACCCC
2201  TGTCACTACA GCCTCACCTC CTACAGCCTT AAGTCCCAGG CCCATGTCTG
2251  CCTGTCCAAG GGCTCAAGAC TTTCTAACTG GGATGTGGTA GAGGGACTGA
2301  AGGTACCTTT GGGGGCAACA GCACCCTAGT TTCATTCTCA ACTCTAGCCC
2351  TGCACACTCA CCTGTGGCAC GGAATGAAAA CAGAGCTTCC CGTGCAAAAA
2401  GGGTCACGCC TCCCACCCCC GCCCCTCCC TGCACCTCCT GTCCTCTCCC
2451  AGTTCATTCC TGGAACCAGC CAGGCCAGGC AACCAGTGGC CCCCAAAGGC
2501  AGGCAGGATC CTCAGGCCCC AGCCGCGGGA GGCTGGAAGG GCTGGCAGAT
2551  CGCTTCCCTC ATCCACCTCC ACCGGTCCAG GTCTTTGCTG CTGTCCCCAG
2601  ACCTCCTGTG ACACCACGCC AGATCACAGG GCACCAGGCC AGAGATAGTC
2651  TTCTTTTTGT CCTTTCTGGC CTCTGGCTAG TCAGTTTTTC ATAGCCTTAC
2701  AGTATCTGGC TTTGTACTGA GAAATAAAAC ACATTTTCAT AAAAAAAAAA
2751  AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2801  AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2851  AA
```

FIGURE 1, page 2 of 5

FEATURES:
5' UTR: 1-56
Start: 57
Stop: 2034
3' UTR: 2037-2852

SPLICE FORM 3:

```
   1  CCTGGTCCTG CGGGTCCAGG ACTGTCCCGC GGGGTTGAGG GAAGGGGCCG
  51  TGCCCGGTGC CAGCCCAGGT GCTCGCGGCC TGGCTCCATG GCCCTGGTCA
 101  CAGTGAGCCG TTCGCCCCCG GGCAGCGGCG CCTCCACGCC CGTGGGGCCC
 151  TGGGACCAGG CGGTCCAGCG AAGGAGTCGA CTCCAGCGAA GGCAGAGCTT
 201  TGCGGTGCTC CGTGGGGCTG TCCTGGGACT GCAGGATGGA GGGGACAATG
 251  ATGATGCAGC AGAGGCCAGT TCTGAGCCAA CAGAGAAGGC CCCGAGTGAG
 301  GAGGAGCTCC ACGGGGACCA GACAGACTTC GGGCAAGGAT CCCAGAGTCC
 351  CCAGAAGCAG GAGGAGCAGA GGCAGCACCT GCACCTCATG GTACAGCTGC
 401  TGAGGCCGCA GGATGACATC CGCCTGGCAG CCCAGCTGGA GGCACCCCGG
 451  CCTCCCCGGC TCCGCTACCT GCTGGTAGTT TCTACACGAG AAGGAGAAGG
 501  TCTGAGCCAG GATGAGACGG TCCTCCTGGG CGTGGATTTC CCTGACAGCA
 551  GCTCCCCCAG CTGCACCCTG GGCCTGGTCT TGCCCCTCTG GAGTGACACC
 601  CAGGTGTACT TAGATGGAGA CGGGGGCTTC AGCGTGACGT CTGGTGGGCA
 651  AAGCCGGATC TTCAAGCCCA TCTCCATCCA GACCATGTGG TCCTCAGAAC
 701  AGGAGCAGAT GGAGCAGGCG ATCCGTGCTG AGCTGTGGAA AGTGTTGGAT
 751  GTCAGTGACC TGGAGAGTGT CACTTCCAAA GAGATCCGCC AGGCTCTGGA
 801  GCTGCGCCTG GGGCTCCCCC TCCAGCAGTA CCGTGACTTC ATCGACAACC
 851  AGATGCTGCT GCTGGTGGCA CAGCGGGACC GAGCCTCCCG CATCTTCCCC
 901  CACCTCTACC TGGGCTCAGA GTGGAACGCA GCAAACCTGG AGGAGCTGCA
 951  GAGGAACAGG GTCACCCACA TCTTGAACAT GGCCCGGGAG ATTGACAACT
1001  TCTACCCTGA GCGCTTCACC TACCACAATG TGCGCCTCTG GGATGAGGAG
1051  TCGGCCCAGC TGCTGCCGCA CTGGAAGGAG ACGCACCGCT TCATTGAGGC
1101  TGCAAGAGCA CAGGGCACCC ACGTGCTGGT CCACTGCAAG ATGGGCGTCA
1151  GCCGCTCAGC GGCCACAGTG CTGGCCTATG CCATGAAGCA GTACGAATGC
1201  AGCCTGGAGC AGGCCCTGCG CCACGTGCAG GAGCTCCGGC CCATCGCCCG
1251  CCCCAACCCT GGCTTCCTGC GCCAGCTGCA GATCTACCAG GGCATCCTGA
1301  CGGCCAGAAC CTGAGGGTGG TGGGGAGGAG AAGGTTGTAG GCATGGAAGA
1351  GAGCCAGGCA GCCCCGAAAG AAGAGCCTGG GGCCACGGGG CACGTATAAA
1401  CCTCCGAGGG GTCATGAGGT CCATCAGTCT TCTGGAGCCC TCCTTGGGAG
1451  CTGGAGAGCA CCTCAGTAGA CCAGTGACAT GCCAGAGGTC TTCTCTTCCC
1501  ACGAGTCTTC ACATGAAGAG CCTCTGCAGC CCTTCCCACA GCTTGCAAGG
1551  ACCAAGGGAG GCCAGCAGGT GGACAGGGGG CCTCAGCCTG CCCTGAAGTC
1601  CCGCCAGTCA GTGGTTACCC TCCAGGGCAG TGCCGTGGTG GCCAACCGGA
1651  CCCAGGCCTT CCAGGAGCAG GAGCAGGGGC AGGGGCAGGG GCAGGGAGAG
1701  CCCTGCATTT CCTCTACGCC CAGGTTCCGG AAGGTGGTGA GACAGGCCAG
1751  CGTGCATGAC AGTGGAGAGG AGGGCGAGGC CTGAGCCCTC ACACATGCCC
1801  ACGCTCCCCT GACACTGAAG AGGATCCACA ACTCCTTGGA GAAACACCCT
1851  CACGTCTGTT GCCGCACACA TTCCTCTCAG CTCCGCCCCA TACCCGTCAC
1901  TACAGCCTCA CCTCCCACCC CTGTCACTAC GGCCTCACCT CCCACCCCTG
1951  TCACTACAGC CTCACCTCCT ACAGCCTTAA GTCCCAGGCC CATGTCTGCC
2001  TGTCCAAGGG CTCAAGACTT CTAACTGGG ATGTGGTAGA GGGACTGAAG
2051  GTACCTTTGG GGGCAACAGC ACCCTAGTTT CATTCTCAAC TCTAGCCCTG
2101  CACACTCACC TGTGGCACGG AATGAAAACA GAGCTTCCCG TGCAAAAAGG
2151  GTCACGCCTC CCACCCCCGC CCCCTCCCTG CACCTCCTGT CCTCTCCCAG
2201  TTCATTCCTG GAACCAGCCA GGCCAGGCAA CCAGTGGCCC CCAAAGGCAG
2251  GCAGGATCCT CAGGCCCCAG CCGCGGGAGG CTGGAAGGGC TGGCAGATCG
2301  CTTCCCTCAT CCACCTCCAC CGGTCCAGGT CTTTGCTGCT GTCCCCAGAC
2351  CTCCTGTGAC ACCACGCCAG ATCACAGGGC ACCAGGCCAG AGATAGTCTT
2401  CTTTTTGTCC TTTCTGGCCT CTGGCTAGTC AGTTTTTCAT AGCCTTACAG
2451  TATCTGGCTT TGTACTGAGA AATAAAACAC ATTTTCATAT TTGGTTAAAA
2501  AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

FEATURES:
5′ UTR: 1-88
Start: 88
Stop: 1311
3′ UTR: 1315-2540

Homologous proteins:
Top 10 BLAST Hits

	Score	E

SPLICE FORM 1:

	Score	E
gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515 >gi|7...	576	e-163
gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase [D...	337	2e-91
gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928 >gi|7...	233	3e-60
gi|7242951|dbj|BAA92536.1| (AB037719) KIAA1298 protein [Homo sa...	143	4e-33
gi|7301242|gb|AAF56372.1| (AE003750) CG6238 gene product [Droso...	124	2e-27
gi|4150963|emb|CAA77232.1| (Y18620) DsPTP1 protein [Arabidopsis...	113	5e-24
gi|9294518|dbj|BAB02780.1| (AB023036) dual-specificity protein ...	113	5e-24
gi|6862915|gb|AAF30304.1|AC018907_4 (AC018907) putative dual-sp...	94	2e-18
gi|6015037|sp|O54838|DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	9e-18
gi|9910432|ref|NP_064570.1| mitogen-activated protein kinase ph...	90	3e-17

SPLICE FORM 2:

gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515 [Homo...	576	e-163
gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase [D...	340	6e-92
gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928 [Homo...	229	1e-58
gi|7242951|dbj|BAA92536.1| (AB037719) KIAA1298 protein [Homo sa...	162	1e-38
gi|9294518|dbj|BAB02780.1| (AB023036) dual-specificity protein ...	113	8e-24
gi|4150963|emb|CAA77232.1| (Y18620) DsPTP1 protein [Arabidopsis...	113	8e-24
gi|4758212|ref|NP_004411.1| dual specificity phosphatase 8 [Hom...	99	3e-19
gi|6679156|ref|NP_032774.1| neuronal tyrosine/threonine phospha...	96	2e-18
gi|6862915|gb|AAF30304.1|AC018907_4 (AC018907) putative dual-sp...	94	6e-18
gi|6015037|sp|O54838|DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17

SPLICE FORM 3:

gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515 [Homo...	410	e-113
gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928 [Homo...	233	7e-60
gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase [D...	224	5e-57
gi|7242951|dbj|BAA92536.1| (AB037719) KIAA1298 protein [Homo sa...	143	5e-33
gi|9294518|dbj|BAB02780.1| (AB023036) dual-specificity protein ...	113	1e-23
gi|4150963|emb|CAA77232.1| (Y18620) DsPTP1 protein [Arabidopsis...	113	1e-23
gi|6862915|gb|AAF30304.1|AC018907_4 (AC018907) putative dual-sp...	94	5e-18
gi|6015037|sp|O54838|DUS5_RAT DUAL SPECIFICITY PROTEIN PHOSPHAT...	92	2e-17
gi|9910432|ref|NP_064570.1| mitogen-activated protein kinase ph...	90	7e-17
gi|9911130|gb|AAA64693.2| (U15932) protein phosphatase [Homo sa...	90	1e-16

BLAST to dbEST:
SPLICE FORM 1:

	Score	E
gi|9807071 /dataset=dbest /taxon=960...	1404	0.0
gi|10317998 /dataset=dbest /taxon=96...	1316	0.0
gi|10151079 /dataset=dbest /taxon=96...	1249	0.0
gi|10401153 /dataset=dbest /taxon=960...	1180	0.0
gi|10329921 /dataset=dbest /taxon=96...	1124	0.0
gi|7632969 /dataset=dbest /taxon=960...	791	0.0
gi|9155111 /dataset=dbest /taxon=9606...	779	0.0
gi|10994242 /dataset=dbest /taxon=96...	450	e-124

FIGURE 1, page 4 of 5

EXPRESSION INFORMATION FOR MODULATORY USE:
SPLICE FORM 1:
library source:
Expression information from BLAST dbEST hits:
gi|9807071   Human Pancreas
gi|10317998   Human colon adenocarcinoma
gi|10151079   Human Pancreas:adenocarcinoma
gi|10401153   Human Pancreas:epitheliod carcinoma
gi|10329921   Human lung: large cell carcinoma
gi|7632969   Human kidney: renal cell carcinoma
gi|9155111   Human Placenta choriocarcinoma
gi|10994242   Human ovary tumor tissue

Expression information from PCR-based tissue screening panels:
Human Brain
Human Fetal brain
Human fetal heart
Human fetal kidney
Human heart
Human kidney
Human uterus
Human thyroid

```
  1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
 51 GGDNDDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEAALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSEQEQ MEQAIRAELW KVLDVSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSLEQAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAR T
```

SPLICE FORM 2:

```
  1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
 51 GGDNDDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WATLQVLHQA CEAALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
251 DLESLRPPSA EPGGSSEQEQ MEQAIRAELW KVLDVSDLES VTSKEIRQAL
301 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
351 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
401 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSLEQAL RHVQELRPIA
451 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVSPEEHPA PEVSTPFPLL
501 PPEPEGGGEE KVVGMEESQA APKEEPGPRP RINLRGVMRS ISLLEPSLEL
551 ESTSETSDMP EVFSSHESSH EEPLQPFPQL ARTKGGQQVD RGPQPALKSR
601 QSVVTLQGSA VVANRTQAFQ EQEQGQGQGQ GEPCISSTPR FRKVVRQASV
651 HDSGEEGEA
```

SPLICE FORM 3:

```
  1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
 51 GGDNDDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
101 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
151 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
201 WSSEQEQMEQ AIRAELWKVL DVSDLESVTS KEIRQALELR LGLPLQQYRD
251 FIDNQMLLLV AQRDRASRIF PHLYLGSEWN AANLEELQRN RVTHILNMAR
301 EIDNFYPERF TYHNVRLWDE ESAQLLPHWK ETHRFIEAAR AQGTHVLVHC
351 KMGVSRSAAT VLAYAMKQYE CSLEQALRHV QELRPIARPN PGFLRQLQIY
401 QGILTART
```

FEATURES:
Functional domains and key regions:
SPLICE FORM 1:
[1] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

            34-37 RRQS

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 6
        1   65-67 TEK
        2   132-134 STR
        3   254-256 SLR
        4   292-294 TSK
        5   395-397 THR
        6   468-470 TAR

FIGURE 2, page 1 of 4

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 6
```
        1       70-73  SEEE
        2      132-135 STRE
        3      140-143 SQDE
        4      266-269 SEQE
        5      286-289 SDLE
        6      292-295 TSKE
```

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

```
               363-369 REIDNFY
```

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 8
```
        1       12-17  GSGAST
        2       43-48  GAVLGL
        3       47-52  GLQDGG
        4      218-223 GLVPGG
        5      223-228 GSALTW
        6      339-344 GSEWNA
        7      416-421 GVSRSA
        8      465-470 GILTAR
```

FIGURE 2, page 2 of 4

BLAST Alignment to Top Hit:
SPLICE FORM 1:
>gi|8923483|ref|NP_060327.1| hypothetical protein FLJ20515
          >gi|7020674|dbj|BAA91228.1| (AK000522) unnamed protein
          product [Homo sapiens]
          Length = 394

  Score = 576 bits (1469), Expect = e-163
  Identities = 290/312 (92%), Positives = 296/312 (93%), Gaps = 1/312 (0%)

Query: 1   MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60
            MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA
Sbjct: 1   MALVTVSRSPPGSGASTPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAEA 60

Query: 61   SSEPTEKAPSEEELHGDQTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120
            SSEPTEKAPSEEELHGDQTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP
Sbjct: 61   SSEPTEKAPSEEELHGDQTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEAP 120

Query: 121 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPLWSDTQVYLDGDGG 180
            RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPLWSDTQVYLDGDGG
Sbjct: 121 RPPRLRYLLVVSTREGEGLSQDETVLLGVDFPDSSSPSCTLGLVLPLWSDTQVYLDGDGG 180

Query: 181 FSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ 240
            FSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ
Sbjct: 181 FSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQERLNSEQ 240

Query: 241 SCLNEWTAMADLESLRPPSAEPGGSSEQEQMEQAIRAELWKVLDV-SDLESVTSKEIRQA 299
            SCLNEWTAMADLESLRPPSAEPGGSSEQEQMEQAIRAELWKVL++ S E+   E+   +
Sbjct: 241 SCLNEWTAMADLESLRPPSAEPGGSSEQEQMEQAIRAELWKVLELESTSETSDMPEVFSS 300

Query: 300 LELRLGLPLQQY 311
            E   PLQ +
Sbjct: 301 HESSHEEPLQPF 312

>gi|6714641|dbj|BAA89534.1| (AB036834) MAP kinase phosphatase
          [Drosophila melanogaster]
          Length = 1045

  Score = 337 bits (854), Expect = 2e-91
  Identities = 204/537 (37%), Positives = 284/537 (51%), Gaps = 81/537 (15%)

Query: 1   MALVTVSRSPPGSGA-STPVGPWDQAVQRRSRLQRRQSFAVLRGAVLGLQDGGDNDDAAE 59
            MALVTV RSP +G+ S G +   R + F +G L L
Sbjct: 1   MALVTVQRSPSVAGSCSNSDGESEDDEGNSKGNDRSECFFAGKGTALVL---------- 49

Query: 60   ASSEPTEKAPSEEELHGDQTDFGQGSQSPQKQEEQRQHLHLMVQLLRPQDDIRLAAQLEA 119
            A +   SE L D T   +QS   + + HL M LL+ +D +++A +LE+
Sbjct: 50   ALKDIPPLTQSERRLSTDSTRSSNSTQS--NNSDIQLHLQSMFYLLQREDTLKMAVKLES 107

Query: 120 PRPPRLRYLLV---------VSTREGEGLSQDETVLLGVDFPDSSSPS------------ 158
             R R RYL++   S R   + +V +G   SS S
Sbjct: 108 QRSNRTRYLVIASRSCCRSGTSDRRRHRIMRHHSVKVGGSAGTKSSTSPAVPTQRQLSVE 167

Query: 159 ------------------------------CTLGL---------VLPLWSDTQVY 174
                                          C LG+   V+P+ +DT ++
Sbjct: 168 QTATEASSKCDKTADKENATAAGDNKNTSGMEESCLLGIDCNERTTIGLVVPILADTTIH 227

Query: 175 LDGDGGFSVTSGGQSRIFKPISIQTMWATLQVLHQACEAALGSGLVPGGSALTWASHYQE 234
            LDGDGGFSV   ++ IFKP+S+Q MW+ LQ LH+ + A +   G +   W S Y+
Sbjct: 228 LDGDGGFSVKVYEKTHIFKPVSVQAMWSALQTLHKVSKKARENNFYASGPSHDWLSSYER 287

```
Query:  235 RLNSEQSCLNEWTAMADLESLRPPSAEP--GGSSEQEQMEQAIRAELWKVLDVSDLESVT 292
            R+ S+QSCLNEW AM  LES RPPS +            E+E+ E  I+ +L  ++    DL+ VT
Sbjct:  288 RIESDQSCLNEWNAMDALESRRPPSPDAIRNKPPEKEETESVIKMKLKAIMMSVDLDEVT 347

Query:  293 SKEIRQALELRLGLPLQQYRDFIDNQMLLLVAQRDRASRIFPHLYLGSEWNAANLEELQR 352
            SK IR  LE  L + L +Y+ FID +ML+++ Q D  ++IF H+YLGSEWNA+NLEELQ+
Sbjct:  348 SKYIRGRLEEILDMDLGEYKSFIDAEMLVILGQMDAPTKIFEHVYLGSEWNASNLEELQK 407

Query:  353 NRVTHILNMAREIDNFYPERFTYHNVRLWDEESAQLLPHWKETHRFIEAARAQGTHVLVH 412
            N V HILN+ REIDNF+P  F Y NVR++D+E   LL +W +T R+I  A+A+G+ VLVH
Sbjct:  408 NGVRHILNVTREIDNFFPGTFEYFNVRVYDDEKTNLLKYWDDTFRYITRAKAEGSKVLVH 467

Query:  413 CKMGVSRSAATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTA 469
            CKMGVSRSA+ V+AYAMK Y+   +QAL HV++ R    +PN  FL QL+ Y G+L A
Sbjct:  468 CKMGVSRSASVVIAYAMKAYQWEFQQALEHVKKRRSCIKPNKNFLNQLETYSGMLDA 524


>gi|8922777|ref|NP_060746.1| hypothetical protein FLJ10928
          >gi|7023283|dbj|BAA91913.1| (AK001790) unnamed protein
          product [Homo sapiens]
          Length = 141

 Score =  233 bits (588), Expect = 3e-60
 Identities = 111/111 (100%), Positives = 111/111 (100%)

Query:  361 MAREIDNFYPERFTYHNVRLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 420
            MAREIDNFYPERFTYHNVRLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS
Sbjct:   31 MAREIDNFYPERFTYHNVRLWDEESAQLLPHWKETHRFIEAARAQGTHVLVHCKMGVSRS 90

Query:  421 AATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTART 471
            AATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTART
Sbjct:   91 AATVLAYAMKQYECSLEQALRHVQELRPIARPNPGFLRQLQIYQGILTART 141
```

```
   1 CGTCCTTCCT GGTCCTGCGG GTCCAGGACT GTCCGCGGGG TTGAGGGAAG
  51 GGGCCGTGCC CGGTGCCAGC CCAGGTGCTC GCGGCCTGGC TCCATGGCCC
 101 TGGTCACAGT GAGCCGTTCG CCCCCGGGCA GCGGCGCCTC CACGCCCGTG
 151 GGGCCCTGGG ACCAGGCGGT CCAGCGAAGG AGTCGACTCC AGCGAAGGCA
 201 GAGCTTTGCG GTGCTCCGTG GGGCTGTCCT GGGACTGCAG GATGGAGGGG
 251 ACAATGATGA TGCAGCAGAG GCCAGTTCTG AGCCAACAGA GAAGGCCCCG
 301 AGTGAGGAGG AGCTCCACGG GGACCAGACA GACTTCGGGC AAGGATCCCA
 351 GAGTCCCCAG AAGCAGGAGG AGCAGAGGCA GCACCTGCAC CTCATGGTAC
 401 AGCTGCTGAG GCCGCAGGAT GACATCCGCC TGGCAGCCCA GCTGGAGGCA
 451 CCCCGGCCTC CCCGGCTCCG CTACCTGCTG GTAGTTTCTA CACGAGAAGG
 501 AGAAGGTCTG AGCCAGGATG AGACGGTCCT CCTGGGCGTG GATTTCCCTG
 551 ACAGCAGCTC CCCCAGCTGC ACCCTGGGCC TGGTCTTGCC CCTCTGGAGT
 601 GACACCCAGG TGTACTTAGA TGGAGACGGG GGCTTCAGCG TGACGTCTGG
 651 TGGGCAAAGC CGGATCTTCA AGCCCATCTC CATCCAGACC ATGTGGGCCA
 701 CACTCCAGGT ATTGCACCAA GCATGTGAGG CAGCTCTAGG CAGCGGCCTT
 751 GTACCGGGTG GCAGTGCCCT CACCTGGGCC AGCCACTACC AGGAGAGACT
 801 GAACTCCGAA CAGAGCTGCC TCAATGAGTG GACGGCTATG GCCGACCTGG
 851 AGTCTCTGCG GCCTCCCAGC GCCGAGCCTG GCGGGTCCTC AGAACAGGAG
 901 CAGATGGAGC AGGCGATCCG TGCTGAGCTG TGGAAAGTGT TGGATGTCAG
 951 TGACCTGGAG AGTGTCACTT CCAAAGAGAT CCGCCAGGCT CTGGAGCTGC
1001 GCCTGGGGCT CCCCCTCCAG CAGTACCGTG ACTTCATCGA CAACCAGATG
1051 CTGCTGCTGG TGGCACAGCG GGACCGAGCC TCCCGCATCT TCCCCCACCT
1101 CTACCTGGGC TCAGAGTGGA ACGCAGCAAA CCTGGAGGAG CTGCAGAGGA
1151 ACAGGGTCAC CCACATCTTG AACATGGCCC GGGAGATTGA CAACTTCTAC
1201 CCTGAGCGCT TCACCTACCA CAATGTGCGC CTCTGGGATG AGGAGTCGGC
1251 CCAGCTGCTG CCGCACTGGA AGGAGACGCA CCGCTTCATT GAGGCTGCAA
1301 GAGCACAGGG CACCCACGTG CTGGTCCACT GCAAGATGGG CGTCAGCCGC
1351 TCAGCGGCCA CAGTGCTGGC CTATGCCATG AAGCAGTACG AATGCAGCCT
1401 GGAGCAGGCC CTGCGCCACG TGCAGGAGCT CCGGCCCATC GCCCGCCCCA
1451 ACCCTGGCTT CCTGCGCCAG CTGCAGATCT ACCAGGGCAT CCTGACGGCC
1501 AGAACCTGAG GGTGGTGGGG AGGAGAAGGT TGTAGGCATG GAAGAGAGCC
1551 AGGCAGCCCC GAAAGAAGAG CCTGGGCCAC GGCCACGTAT AAACCTCCGA
1601 GGGGTCATGA GGTCCATCAG TCTTCTGGAG CCCTCCTTGG AGCTGGAGAG
1651 CACCTCAGAG ACCAGTGACA TGCCAGAGGT CTTCTCTTCC CACGAGTCTT
1701 CACATGAAGA GCCTCTGCAG CCCTTCCCAC AGCTTGCAAG GACCAAGGGA
1751 GGCCAGCAGG TGGACAGGGG GCCTCAGCCT GCCCTGAAGT CCCGCCAGTC
1801 AGTGGTTACC CTCCAGGGCA GTGCCGTGGT GGCCAACCGG ACCCAGGCCT
1851 TCCAGGAGCA GGAGCAGGGG CAGGGGCAGG GGCAGGGAGA GCCCTGCATT
1901 TCCTCTACGC CCAGGTTCCG GAAGGTGGTG AGACAGGCCA GCGTGCATGA
1951 CAGTGGAGAG GAGGGCGAGG CCTGAGCCCT CACACATGCC CACGCTCCCC
2001 TGACACTGAA GAGGATCCAC AACTCCTTGG AGAAACACCC TCACGTCTGT
2051 TGCCGCACAC ATTCCTCTCA GCTCCGCCCC ATACCCGTCA CTACAGCCTC
2101 ACCTCCCACC CCTGTCACTA CGGCCTCACC TCCCACCCCT GTCACTACAG
2151 CCTCACCTCC TACAGCCTTA AGTCCCAGGC CCATGTCTGC CTGTCCAAGG
2201 GCTCAAGACT TTCTAACTGG GATGTGGTAG AGGGACTGAA GGTACCTTTG
2251 GGGGCAACAG CACCCTAGTT TCATTCTCAA CTCTAGCCCT GCACACTCAC
2301 CTGTGGCACG GAATGAAAAC AGAGCTTCCC GTGCAAAAAG GGTCACGCCT
2351 CCCACCCCCG CCCCCTCCCT GCACCTCCTG TCCTCTCCCA GTTCATTCCT
2401 GGAACCAGCC AGGCCAGGCA ACCAGTGGCC CCCAAAGGCA GGCAGGATCC
2451 TCAGGCCCCA GCCGCGGGAG GCTGGAAGGG CTGGCAGATC GCTTCCCTCA
2501 TCCACCTCCA CCGGTCCAGG TCTTTGCTGC TGTCCCCAGA CCTCCTGTGA
2551 CACCACGCCA GATCACAGGG CACCAGGCCA GAGATAGTCT TCTTTTTGTC
2601 CTTTCTGGCC TCTGGCTAGT CAGTTTTTCA TAGCCTTACA GTATCTGGCT
2651 TTGTACTGAG AAATAAAACA CATTTTCATA AAAAAAAAAA AAAAAAAAAA
2701 AAAA
```

FEATURES:

Start: 94
Exon: 94-1506
Stop: 1507

CHROMOSOME MAP POSITION:
Bac accession number: AP001885
Chromosome #: 11

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
577	G	A	Exon	162	G	S
1451	G	A	Exon	453	S	N
2641	G	A	Beyond ORF(3')			

Context:

DNA
Position
577   TCTGAGCCAACAGAGAAGGCCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGACTTC
        GGGCAAGGATCCCAGAGTCCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTCATG
        GTACAGCTGCTGAGGCCGCAGGATGACATCCGCCTGGCAGCCCAGCTGGAGGCACCCCGG
        CCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGCCAG
        GATGAGACGGTCCTCCTGGGCGTGGATTTCCCTGACAGCAGCTCCCCCAGCTGCACCCTG
        [G,A]
        GCCTGGTCTTGCCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGCTTCA
        GCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATGTGGG
        CCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTACCGG
        GTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAGAGCT
        GCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCCAGCGCCGAGC

1451   ACAGGGTCACCCACATCTTGAACATGGCCCGGGAGATTGACAACTTCTACCCTGAGCGCT
        TCACCTACCACAATGTGCGCCTCTGGGATGAGGAGTCGGCCCAGCTGCTGCCGCACTGGA
        AGGAGACGCACCGCTTCATTGAGGCTGCAAGAGCACAGGGCACCCACGTGCTGGTCCACT
        GCAAGATGGGCGTCAGCCGCTCAGCGGCCACAGTGCTGGCCTATGCCATGAAGCAGTACG
        AATGCAGCCTGGAGCAGGCCCTGCGCCACGTGCAGGAGCTCCGGCCCATCGCCCGCCCCA
        [G,A]
        CCCTGGCTTCCTGCGCCAGCTGCAGATCTACCAGGGCATCCTGACGGCCAGAACCTGAGG
        GTGGTGGGGAGGAGAAGGTTGTAGGCATGGAAGAGAGCCAGGCAGCCCCGAAAGAAGAGC
        CTGGGCCACGGCCACGTATAAACCTCCGAGGGGTCATGAGGTCCATCAGTCTTCTGGAGC
        CCTCCTTGGAGCTGGAGAGCACCTCAGAGACCAGTGACATGCCAGAGGTCTTCTCTTCCC
        ACGAGTCTTCACATGAAGAGCCTCTGCAGCCCTTCCCACAGCTTGCAAGGACCAAGGGAG

2641   GGTCACGCCTCCCACCCCCGCCCCCTCCCTGCACCTCCTGTCCTCTCCCAGTTCATTCCT
        GGAACCAGCCAGGCCAGGCAACCAGTGGCCCCCAAAGGCAGGCAGGATCCTCAGGCCCCA
        GCCGCGGGGAGGCTGGAAGGGCTGGCAGATCGCTTCCCTCATCCACCTCCACCGGTCCAGG
        TCTTTGCTGCTGTCCCCAGACCTCCTGTGACACCACGCCAGATCACAGGGCACCAGGCCA
        GAGATAGTCTTCTTTTTGTCCTTTCTGGCCTCTGGCTAGTCAGTTTTTTCATAGCCTTACA
        [G,A]
        TATCTGGCTTTGTACTGAGAAATAAAACACATTTTCATAAAAAAAAAAAAAAAAAAAAAA
        AAA

GENE STRUCTURE MODEL:
SPLICE FORM 2   5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12-e13-e14-3'
SPLICE FORM 1   5'-e1-e2-e3-e4-e5-e6-e7-e8-e9-e10-e11-e12---------3'
SPLICE FORM 3   5'-e1-e2-e3-e4-e5-e6----e8-e9-e10-e11-e12---------3'

MULTIPLE ALIGNMENT OF CDNA SEQUENCES:
SPLICE FORM 2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~TG GTTGAGGGAA
SPLICE FORM 1 CGTCCTTCCT GGTCCTGCGG GTCCAGGACT GT.CCGCGGG GTTGAGGGAA
SPLICE FORM 3 ~~~~~~~CCT GGTCCTGCGG GTCCAGGACT GTCCCGCGGG GTTGAGGGAA

                   51   100
SPLICE FORM 2 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC

FIGURE 3, page 2 of 8

```
SPLICE FORM 1 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC
SPLICE FORM 3 GGGGCCGTGC CCGGTGCCAG CCCAGGTGCT CGCGGCCTGG CTCCATGGCC


                101                                            150
SPLICE FORM 2 CTGGTCACAG TGAGCCGTTC GCCCCCGGGC AGCGGCGCCT CCACGCCCGT
SPLICE FORM 1 CTGGTCACAG TGAGCCGTTC GCCCCCGGGC AGCGGCGCCT CCACGCCCGT
SPLICE FORM 3 CTGGTCACAG TGAGCCGTTC GCCCCCGGGC AGCGGCGCCT CCACGCCCGT


                151                                            200
SPLICE FORM 2 GGGGCCCTGG GACCAGGCGG TCCAGCGAAG GAGTCGACTC CAGCGAAGGC
SPLICE FORM 1 GGGGCCCTGG GACCAGGCGG TCCAGCGAAG GAGTCGACTC CAGCGAAGGC
SPLICE FORM 3 GGGGCCCTGG GACCAGGCGG TCCAGCGAAG GAGTCGACTC CAGCGAAGGC


                201                                            250
SPLICE FORM 2 AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA GGATGGAGGG
SPLICE FORM 1 AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA GGATGGAGGG
SPLICE FORM 3 AGAGCTTTGC GGTGCTCCGT GGGGCTGTCC TGGGACTGCA GGATGGAGGG


                251                                            300
SPLICE FORM 2 GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
SPLICE FORM 1 GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC
SPLICE FORM 3 GACAATGATG ATGCAGCAGA GGCCAGTTCT GAGCCAACAG AGAAGGCCCC


                301                                            350
SPLICE FORM 2 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC
SPLICE FORM 1 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC
SPLICE FORM 3 GAGTGAGGAG GAGCTCCACG GGGACCAGAC AGACTTCGGG CAAGGATCCC


                351                                            400
SPLICE FORM 2 AGAGTCCCCA GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA
SPLICE FORM 1 AGAGTCCCCA GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA
SPLICE FORM 3 AGAGTCCCCA GAAGCAGGAG GAGCAGAGGC AGCACCTGCA CCTCATGGTA


                401                                            450
SPLICE FORM 2 CAGCTGCTGA GGCCGCAGGA TGACATCCGC CTGGCAGCCC AGCTGGAGGC
SPLICE FORM 1 CAGCTGCTGA GGCCGCAGGA TGACATCCGC CTGGCAGCCC AGCTGGAGGC
SPLICE FORM 3 CAGCTGCTGA GGCCGCAGGA TGACATCCGC CTGGCAGCCC AGCTGGAGGC


                451                                            500
SPLICE FORM 2 ACCCCGGCCT CCCCGGCTCC GCTACCTGCT GGTAGTTTCT ACACGAGAAG
SPLICE FORM 1 ACCCCGGCCT CCCCGGCTCC GCTACCTGCT GGTAGTTTCT ACACGAGAAG
SPLICE FORM 3 ACCCCGGCCT CCCCGGCTCC GCTACCTGCT GGTAGTTTCT ACACGAGAAG


                501                                            550
SPLICE FORM 2 GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT GGATTTCCCT
SPLICE FORM 1 GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT GGATTTCCCT
SPLICE FORM 3 GAGAAGGTCT GAGCCAGGAT GAGACGGTCC TCCTGGGCGT GGATTTCCCT


                551                                            600
SPLICE FORM 2 GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
SPLICE FORM 1 GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG
SPLICE FORM 3 GACAGCAGCT CCCCCAGCTG CACCCTGGGC CTGGTCTTGC CCCTCTGGAG


                601                                            650
SPLICE FORM 2 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG
SPLICE FORM 1 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG
SPLICE FORM 3 TGACACCCAG GTGTACTTAG ATGGAGACGG GGGCTTCAGC GTGACGTCTG


                651                                            700
SPLICE FORM 2 GTGGGCAAAG CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC
SPLICE FORM 1 GTGGGCAAAG CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGTGGGCC
SPLICE FORM 3 GTGGGCAAAG CCGGATCTTC AAGCCCATCT CCATCCAGAC CATGT.....
```

FIGURE 3, page 3 of 8

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                701                                                      750
SPLICE FORM 2 ACACTCCAGG TATTGCACCA AGCATGTGAG GCAGCTCTAG GCAGCGGCCT
SPLICE FORM 1 ACACTCCAGG TATTGCACCA AGCATGTGAG GCAGCTCTAG GCAGCGGCCT
SPLICE FORM 3 .......... .......... .......... .......... ..........

                751                                                      800
SPLICE FORM 2 TGTACCGGGT GGCAGTGCCC TCACCTGGGC CAGCCACTAC CAGGAGAGAC
SPLICE FORM 1 TGTACCGGGT GGCAGTGCCC TCACCTGGGC CAGCCACTAC CAGGAGAGAC
SPLICE FORM 3 .......... .......... .......... .......... ..........

                801                                                      850
SPLICE FORM 2 TGAACTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT GGCCGACCTG
SPLICE FORM 1 TGAACTCCGA ACAGAGCTGC CTCAATGAGT GGACGGCTAT GGCCGACCTG
SPLICE FORM 3 .......... .......... .......... .......... ..........

                851                                                      900
SPLICE FORM 2 GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
SPLICE FORM 1 GAGTCTCTGC GGCCTCCCAG CGCCGAGCCT GGCGGGTCCT CAGAACAGGA
SPLICE FORM 3 .......... .......... .......... ....GGTCCT CAGAACAGGA

                901                                                      950
SPLICE FORM 2 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA
SPLICE FORM 1 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA
SPLICE FORM 3 GCAGATGGAG CAGGCGATCC GTGCTGAGCT GTGGAAAGTG TTGGATGTCA

                951                                                     1000
SPLICE FORM 2 GTGACCTGGA GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG
SPLICE FORM 1 GTGACCTGGA GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG
SPLICE FORM 3 GTGACCTGGA GAGTGTCACT TCCAAAGAGA TCCGCCAGGC TCTGGAGCTG

                1001                                                    1050
SPLICE FORM 2 CGCCTGGGGC TCCCCCTCCA GCAGTACCGT GACTTCATCG ACAACCAGAT
SPLICE FORM 1 CGCCTGGGGC TCCCCCTCCA GCAGTACCGT GACTTCATCG ACAACCAGAT
SPLICE FORM 3 CGCCTGGGGC TCCCCCTCCA GCAGTACCGT GACTTCATCG ACAACCAGAT

                1051                                                    1100
SPLICE FORM 2 GCTGCTGCTG GTGGCACAGC GGGACCGAGC CTCCCGCATC TTCCCCCACC
SPLICE FORM 1 GCTGCTGCTG GTGGCACAGC GGGACCGAGC CTCCCGCATC TTCCCCCACC
SPLICE FORM 3 GCTGCTGCTG GTGGCACAGC GGGACCGAGC CTCCCGCATC TTCCCCCACC

                1101                                                    1150
SPLICE FORM 2 TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA GCTGCAGAGG
SPLICE FORM 1 TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA GCTGCAGAGG
SPLICE FORM 3 TCTACCTGGG CTCAGAGTGG AACGCAGCAA ACCTGGAGGA GCTGCAGAGG

                1151                                                    1200
SPLICE FORM 2 AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
SPLICE FORM 1 AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA
SPLICE FORM 3 AACAGGGTCA CCCACATCTT GAACATGGCC CGGGAGATTG ACAACTTCTA

                1201                                                    1250
SPLICE FORM 2 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG
SPLICE FORM 1 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG
SPLICE FORM 3 CCCTGAGCGC TTCACCTACC ACAATGTGCG CCTCTGGGAT GAGGAGTCGG

                1251                                                    1300
SPLICE FORM 2 CCCAGCTGCT GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA
SPLICE FORM 1 CCCAGCTGCT GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA
SPLICE FORM 3 CCCAGCTGCT GCCGCACTGG AAGGAGACGC ACCGCTTCAT TGAGGCTGCA

                1301                                                    1350
SPLICE FORM 2 AGAGCACAGG GCACCCACGT GCTGGTCCAC TGCAAGATGG GCGTCAGCCG
SPLICE FORM 1 AGAGCACAGG GCACCCACGT GCTGGTCCAC TGCAAGATGG GCGTCAGCCG
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```
SPLICE FORM 3  AGAGCACAGG  GCACCCACGT  GCTGGTCCAC  TGCAAGATGG  GCGTCAGCCG


              1351                                            1400
SPLICE FORM 2  CTCAGCGGCC  ACAGTGCTGG  CCTATGCCAT  GAAGCAGTAC  GAATGCAGCC
SPLICE FORM 1  CTCAGCGGCC  ACAGTGCTGG  CCTATGCCAT  GAAGCAGTAC  GAATGCAGCC
SPLICE FORM 3  CTCAGCGGCC  ACAGTGCTGG  CCTATGCCAT  GAAGCAGTAC  GAATGCAGCC


              1401                                            1450
SPLICE FORM 2  TGGAGCAGGC  CCTGCGCCAC  GTGCAGGAGC  TCCGGCCCAT  CGCCCGCCCC
SPLICE FORM 1  TGGAGCAGGC  CCTGCGCCAC  GTGCAGGAGC  TCCGGCCCAT  CGCCCGCCCC
SPLICE FORM 3  TGGAGCAGGC  CCTGCGCCAC  GTGCAGGAGC  TCCGGCCCAT  CGCCCGCCCC


              1451                                            1500
SPLICE FORM 2  AACCCTGGCT  TCCTGCGCCA  GCTGCAGATC  TACCAGGGCA  TCCTGACGGC
SPLICE FORM 1  AACCCTGGCT  TCCTGCGCCA  GCTGCAGATC  TACCAGGGCA  TCCTGACG..
SPLICE FORM 3  AACCCTGGCT  TCCTGCGCCA  GCTGCAGATC  TACCAGGGCA  TCCTGACG..


              1501                                            1550
SPLICE FORM 2  CAGCCGCCAG  AGCCATGTCT  GGGAGCAGAA  AGTGGGTGGG  GTCTCCCCAG
SPLICE FORM 1  ..........  ..........  ..........  ..........  ..........
SPLICE FORM 3  ..........  ..........  ..........  ..........  ..........


              1551                                            1600
SPLICE FORM 2  AGGAGCACCC  AGCCCCTGAA  GTCTCTACAC  CATTCCCACT  TCTTCCGCCA
SPLICE FORM 1  ..........  ..........  ..........  ..........  ......GCCA
SPLICE FORM 3  ..........  ..........  ..........  ..........  ......GCCA


              1601                                            1650
SPLICE FORM 2  GAACCTGAGG  GTGGTGGGGA  GGAGAAGGTT  GTAGGCATGG  AAGAGAGCCA
SPLICE FORM 1  GAACCTGAGG  GTGGTGGGGA  GGAGAAGGTT  GTAGGCATGG  AAGAGAGCCA
SPLICE FORM 3  GAACCTGAGG  GTGGTGGGGA  GGAGAAGGTT  GTAGGCATGG  AAGAGAGCCA


              1651                                            1700
SPLICE FORM 2  GGCAGCCCCG  AAAGAAGAGC  CTGGG..CCA  CGGCCACGTA  TAAACCTCCG
SPLICE FORM 1  GGCAGCCCCG  AAAGAAGAGC  CTGGG..CCA  CGGCCACGTA  TAAACCTCCG
SPLICE FORM 3  GGCAGCCCCG  AAAGAAGAGC  CTGGGGCCAC  GGGGCACGTA  TAAACCTCCG


              1701                                            1750
SPLICE FORM 2  AGGGGTCATG  AGGTCCATCA  GTCTTCTGGA  GCCCTCCTT.  GGAGCTGGAG
SPLICE FORM 1  AGGGGTCATG  AGGTCCATCA  GTCTTCTGGA  GCCCTCCTT.  GGAGCTGGAG
SPLICE FORM 3  AGGGGTCATG  AGGTCCATCA  GTCTTCTGGA  GCCCTCCTTG  GGAGCTGGAG


              1751                                            1800
SPLICE FORM 2  AGCACCTCAG  .AGACCAGTG  ACATGCCAGA  GGTCTTCTCT  TCCCACGAGT
SPLICE FORM 1  AGCACCTCAG  .AGACCAGTG  ACATGCCAGA  GGTCTTCTCT  TCCCACGAGT
SPLICE FORM 3  AGCACCTCAG  TAGACCAGTG  ACATGCCAGA  GGTCTTCTCT  TCCCACGAGT


              1801                                            1850
SPLICE FORM 2  CTTCACATGA  AGAGCCTCTG  CAGCCCTTCC  CACAGCTTGC  AAGGACCAAG
SPLICE FORM 1  CTTCACATGA  AGAGCCTCTG  CAGCCCTTCC  CACAGCTTGC  AAGGACCAAG
SPLICE FORM 3  CTTCACATGA  AGAGCCTCTG  CAGCCCTTCC  CACAGCTTGC  AAGGACCAAG


              1851                                            1900
SPLICE FORM 2  GGAGGCCAGC  AGGTGGACAG  GGGGCCTCAG  CCTGCCCTGA  AGTCCCGCCA
SPLICE FORM 1  GGAGGCCAGC  AGGTGGACAG  GGGGCCTCAG  CCTGCCCTGA  AGTCCCGCCA
SPLICE FORM 3  GGAGGCCAGC  AGGTGGACAG  GGGGCCTCAG  CCTGCCCTGA  AGTCCCGCCA


              1901                                            1950
SPLICE FORM 2  GTCAGTGGTT  ACCCTCCAGG  GCAGTGCCGT  GGTGGCCAAC  CGGACCCAGG
SPLICE FORM 1  GTCAGTGGTT  ACCCTCCAGG  GCAGTGCCGT  GGTGGCCAAC  CGGACCCAGG
SPLICE FORM 3  GTCAGTGGTT  ACCCTCCAGG  GCAGTGCCGT  GGTGGCCAAC  CGGACCCAGG


              1951                                            2000
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FIGURE 3, page 5 of 8

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SPLICE FORM 2 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
SPLICE FORM 1 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC
SPLICE FORM 3 CCTTCCAGGA GCAGGAGCAG GGGCAGGGGC AGGGGCAGGG AGAGCCCTGC


                2001                                            2050
SPLICE FORM 2 ATTTCCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
SPLICE FORM 1 ATTTCCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA
SPLICE FORM 3 ATTTCCTCTA CGCCCAGGTT CCGGAAGGTG GTGAGACAGG CCAGCGTGCA


                2051                                            2100
SPLICE FORM 2 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCACGCTC
SPLICE FORM 1 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCACGCTC
SPLICE FORM 3 TGACAGTGGA GAGGAGGGCG AGGCCTGAGC CCTCACACAT GCCCACGCTC


                2101                                            2150
SPLICE FORM 2 CCCTGACACT GAAGAGGATC CACAACTCCT TGGAGAAACA CCCTCACGTC
SPLICE FORM 1 CCCTGACACT GAAGAGGATC CACAACTCCT TGGAGAAACA CCCTCACGTC
SPLICE FORM 3 CCCTGACACT GAAGAGGATC CACAACTCCT TGGAGAAACA CCCTCACGTC


                2151                                            2200
SPLICE FORM 2 TGTTGCCGCA CACATTCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
SPLICE FORM 1 TGTTGCCGCA CACATTCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC
SPLICE FORM 3 TGTTGCCGCA CACATTCCTC TCAGCTCCGC CCCATACCCG TCACTACAGC


                2201                                            2250
SPLICE FORM 2 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
SPLICE FORM 1 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA
SPLICE FORM 3 CTCACCTCCC ACCCCTGTCA CTACGGCCTC ACCTCCCACC CCTGTCACTA


                2251                                            2300
SPLICE FORM 2 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
SPLICE FORM 1 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA
SPLICE FORM 3 CAGCCTCACC TCCTACAGCC TTAAGTCCCA GGCCCATGTC TGCCTGTCCA


                2301                                            2350
SPLICE FORM 2 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
SPLICE FORM 1 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT
SPLICE FORM 3 AGGGCTCAAG ACTTTCTAAC TGGGATGTGG TAGAGGGACT GAAGGTACCT


                2351                                            2400
SPLICE FORM 2 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
SPLICE FORM 1 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT
SPLICE FORM 3 TTGGGGGCAA CAGCACCCTA GTTTCATTCT CAACTCTAGC CCTGCACACT


                2401                                            2450
SPLICE FORM 2 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG
SPLICE FORM 1 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG
SPLICE FORM 3 CACCTGTGGC ACGGAATGAA AACAGAGCTT CCCGTGCAAA AAGGGTCACG


                2451                                            2500
SPLICE FORM 2 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
SPLICE FORM 1 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT
SPLICE FORM 3 CCTCCCACCC CCGCCCCCTC CCTGCACCTC CTGTCCTCTC CCAGTTCATT


                2501                                            2550
SPLICE FORM 2 CCTGGAACCA GCCAGGCCAG GCAACCAGTG GCCCCCAAAG GCAGGCAGGA
SPLICE FORM 1 CCTGGAACCA GCCAGGCCAG GCAACCAGTG GCCCCCAAAG GCAGGCAGGA
SPLICE FORM 3 CCTGGAACCA GCCAGGCCAG GCAACCAGTG GCCCCCAAAG GCAGGCAGGA


                2551                                            2600
SPLICE FORM 2 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
SPLICE FORM 1 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
SPLICE FORM 3 TCCTCAGGCC CCAGCCGCGG GAGGCTGGAA GGGCTGGCAG ATCGCTTCCC
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          2601                                                   2650
SPLICE FORM 2 TCATCCACCT CCACCGGTCC AGGTCTTTGC TGCTGTCCCC AGACCTCCTG
SPLICE FORM 1 TCATCCACCT CCACCGGTCC AGGTCTTTGC TGCTGTCCCC AGACCTCCTG
SPLICE FORM 3 TCATCCACCT CCACCGGTCC AGGTCTTTGC TGCTGTCCCC AGACCTCCTG


          2651                                                   2700
SPLICE FORM 2 TGACACCACG CCAGATCACA GGGCACCAGG CCAGAGATAG TCTTCTTTTT
SPLICE FORM 1 TGACACCACG CCAGATCACA GGGCACCAGG CCAGAGATAG TCTTCTTTTT
SPLICE FORM 3 TGACACCACG CCAGATCACA GGGCACCAGG CCAGAGATAG TCTTCTTTTT


          2701                                                   2750
SPLICE FORM 2 GTCCTTTCTG GCCTCTGGCT AGTCAGTTTT TCATAGCCTT ACAGTATCTG
SPLICE FORM 1 GTCCTTTCTG GCCTCTGGCT AGTCAGTTTT TCATAGCCTT ACAGTATCTG
SPLICE FORM 3 GTCCTTTCTG GCCTCTGGCT AGTCAGTTTT TCATAGCCTT ACAGTATCTG


          2751                                                   2800
SPLICE FORM 2 GCTTTGTACT GAGAAATAAA ACACATTTTC ATAAAAAAAA AAAAAAAAAA
SPLICE FORM 1 GCTTTGTACT GAGAAATAAA ACACATTTTC ATAAAAAAAA AAAAAAAAAA
SPLICE FORM 3 GCTTTGTACT GAGAAATAAA ACACATTTTC ATATTTGGTT AAAAAAAAAA


          2801                                                   2850
SPLICE FORM 2 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
SPLICE FORM 1 AAAAAAA~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
SPLICE FORM 3 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA~~~~~~ ~~~~~~~~~~


          2851                                              2894
SPLICE FORM 2 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA
SPLICE FORM 1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
SPLICE FORM 3 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~
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MULTIPLE ALIGNMENT OF PEPTIDE SEQUENCES:
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SPLICE FORM 2 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
SPLICE FORM 1 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD
SPLICE FORM 3 MALVTVSRSP PGSGASTPVG PWDQAVQRRS RLQRRQSFAV LRGAVLGLQD


          51                                                   100
SPLICE FORM 2 GGDNDDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
SPLICE FORM 1 GGDNDDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL
SPLICE FORM 3 GGDNDDAAEA SSEPTEKAPS EEELHGDQTD FGQGSQSPQK QEEQRQHLHL


          101                                                  150
SPLICE FORM 2 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
SPLICE FORM 1 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD
SPLICE FORM 3 MVQLLRPQDD IRLAAQLEAP RPPRLRYLLV VSTREGEGLS QDETVLLGVD


          151                                                  200
SPLICE FORM 2 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
SPLICE FORM 1 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM
SPLICE FORM 3 FPDSSSPSCT LGLVLPLWSD TQVYLDGDGG FSVTSGGQSR IFKPISIQTM


          201                                                  250
SPLICE FORM 2 WATLQVLHQA CEAALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
SPLICE FORM 1 WATLQVLHQA CEAALGSGLV PGGSALTWAS HYQERLNSEQ SCLNEWTAMA
SPLICE FORM 3 W......... .......... .......... .......... ..........


          251                                                  300
SPLICE FORM 2 DLESLRPPSA EPGGSSEQEQ MEQAIRAELW KVLDVSDLES VTSKEIRQAL
SPLICE FORM 1 DLESLRPPSA EPGGSSEQEQ MEQAIRAELW KVLDVSDLES VTSKEIRQAL
SPLICE FORM 3 .......... ....SSEQEQ MEQAIRAELW KVLDVSDLES VTSKEIRQAL


          301                                                  350
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FIGURE 3, page 7 of 8

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SPLICE FORM 2 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
SPLICE FORM 1 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL
SPLICE FORM 3 ELRLGLPLQQ YRDFIDNQML LLVAQRDRAS RIFPHLYLGS EWNAANLEEL


              351                                             400
SPLICE FORM 2 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
SPLICE FORM 1 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE
SPLICE FORM 3 QRNRVTHILN MAREIDNFYP ERFTYHNVRL WDEESAQLLP HWKETHRFIE


              401                                             450
SPLICE FORM 2 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSLEQAL RHVQELRPIA
SPLICE FORM 1 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSLEQAL RHVQELRPIA
SPLICE FORM 3 AARAQGTHVL VHCKMGVSRS AATVLAYAMK QYECSLEQAL RHVQELRPIA


              451                                             500
SPLICE FORM 2 RPNPGFLRQL QIYQGILTAS RQSHVWEQKV GGVSPEEHPA PEVSTPFPLL
SPLICE FORM 1 RPNPGFLRQL QIYQGILTAR T~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
SPLICE FORM 3 RPNPGFLRQL QIYQGILTAR T~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~


              501                                             550
SPLICE FORM 2 PPEPEGGGEE KVVGMEESQA APKEEPGPRP RINLRGVMRS ISLLEPSLEL
SPLICE FORM 1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
SPLICE FORM 3 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~


              551                                             600
SPLICE FORM 2 ESTSETSDMP EVFSSHESSH EEPLQPFPQL ARTKGGQQVD RGPQPALKSR
SPLICE FORM 1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
SPLICE FORM 3 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~


              601                                             650
SPLICE FORM 2 QSVVTLQGSA VVANRTQAFQ EQEQGQGQGQ GEPCISSTPR FRKVVRQASV
SPLICE FORM 1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
SPLICE FORM 3 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~


              651
SPLICE FORM 2 HDSGEEGEA
SPLICE FORM 1 ~~~~~~~~~
SPLICE FORM 3 ~~~~~~~~~
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FIGURE 3, page 8 of 8